

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:40:41 ; Search time 12.7349 Seconds

(Without alignments)  
837.928 Million cell updates/sec

Title: US-09-622-613B-17

Perfect score: 606

Sequence: 1 MQMWFQOKHIINTPIICN.....ICVKEQNPVHFAGIGRCP 111

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : FIR\_73:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582.5	96.1	111	2 A27121	ribonuclease-relat
2	449	74.1	111	1 JX0120	ribonuclease-relat
3	368	60.7	111	2 JX0085	pancreatic ribonuc
4	268.5	44.3	104	2 A39035	ribonuclease-relat
5	129.5	21.4	124	1 NRMHR	pancreatic ribonuc
6	129.5	21.4	145	1 A35932	angiogenin precurs
7	127.5	21.0	167	2 S20066	pancreatic-type ri
8	126.5	20.9	124	1 NRRG	pancreatic ribonuc
9	125.5	20.7	119	2 SA1111	pancreatic ribonuc
10	116.5	9.2	124	1 NRPRI	pancreatic ribonuc
11	116	9.1	122	1 NRRGR	pancreatic ribonuc
12	114.5	8.9	128	1 NRCM	pancreatic ribonuc
13	114.5	8.9	149	1 NRRMS	pancreatic ribonuc
14	113.5	8.7	123	1 A43825	angiogenin - pig
15	112.5	8.6	128	1 NRCGP	pancreatic ribonuc
16	111.5	8.4	128	1 NRCM	pancreatic ribonuc
17	110.5	8.2	124	1 NRCM	pancreatic ribonuc
18	110.5	8.2	124	1 NRCMB	pancreatic ribonuc
19	110.5	8.2	124	1 NRCMB	pancreatic ribonuc
20	110.5	8.2	128	1 NRRS	pancreatic ribonuc
21	108.5	7.9	124	2 S08549	ribonuclease - dom
22	108	7.8	125	1 A32474	angiogenin (valida
23	107.5	7.7	124	1 NRDEN	angiogenin precurs
24	107	7.7	147	1 NRRHOG	angiogenin precurs
25	106.5	7.6	124	1 NRRG	pancreatic ribonuc
26	106.5	7.6	124	1 NRRDEO	pancreatic ribonuc
27	106	7.5	125	1 HA3825	angiogenin - rabbi
28	105.5	7.4	130	2 S22808	pancreatic ribonuc
29	104.5	7.2	124	1 NRRBO	pancreatic ribonuc

30	104.5	7.2	124	1 NRRB	pancreatic ribonuc
31	104.5	7.2	124	1 NRRKN	pancreatic ribonuc
32	104.5	7.2	124	2 S07141	pancreatic ribonuc
33	104.5	7.2	124	2 J05560	pancreatic ribonuc
34	104.5	7.2	150	1 NRRBO	pancreatic ribonuc
35	104.5	7.2	158	2 161900	pancreatic ribonuc
36	103.5	7.1	124	1 NRRSH	pancreatic ribonuc
37	102.5	6.9	119	2 JX0115	pancreatic ribonuc
38	102.5	6.9	124	1 NRRB	pancreatic ribonuc
39	102.5	6.9	152	1 NRRP	pancreatic ribonuc
40	100.5	6.6	124	1 NRRP	pancreatic ribonuc
41	100.5	6.6	125	4 A47498	pancreatic ribonuc
42	100.5	6.6	150	1 NRRBOS	pancreatic ribonuc
43	98.5	6.3	124	1 NRRG	pancreatic ribonuc
44	98.5	6.3	124	1 NRRG	pancreatic ribonuc
45	98	6.2	125	2 S04503	pancreatic ribonuc

## ALIGNMENTS

## RESULT 1

A27121  
ribonuclease-related sialic acid-binding lectin - bullfrog  
C:Species: Rana catesbeiana (bullfrog)  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 30-Jun-1993  
C:Accession: A27121  
R:Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayan  
Biochemistry 26, 2189-2194, 1987  
A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)  
A:Reference number: A27121; MUID:87299649; PMID:3304421  
A:Accession: A27121  
A:Molecule type: protein  
A:Residues: 1111 <TR>  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: lectin

Query Match  
Best Local Similarity 97.3%; Score 582.5; DB 2; Length 111;  
Matches 108; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

OY	2 QNMATFOOKHIINTPII-CNTIMDNIIYVGQCKRVTFIISATYKATCTGVINNV 60
DB	1 ENMATFOOKHIINTPIICNTIMDNIIYVGQCKRVTFIISATYKATCTGVINNV 60
OY	61 LSTRFOULNCTRTSTIRPCPYSSRTETNYICVKEQNPVHFAGIGRCP 111
DB	61 LSTRFOULNCTRTSTIRPCPYSSRTETNYICVKEQNPVHFAGIGRCP 111

## RESULT 2

JX0120  
ribonuclease-related sialic acid-binding lectin - Japanese frog  
C:Species: Rana japonica (Japanese frog)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: JX0120  
R:Kamitaya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayana  
J. Biochem. 108, 139-143, 1990  
A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.  
A:Reference number: JX0120; MUID:91035319; PMID:2229005  
A:Accession: JX0120  
A:Molecule type: protein  
A:Residues: 1111 <KAM>  
A:Experimental source: egg  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: lectin; pyroglyutamic acid  
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match  
Best Local Similarity 74.1%; Score 449; DB 1; Length 111;  
Matches 86; Conservative 7; Mismatches 16; Indels 2; Gaps 2;



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C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental

Query Match          20.9%   Score 126.5 : DB 1 : Length 124:
Best Local Similarity 30.7%   Pred. No. 9.7e+06:
Matches      35:  Conservative    19:  Mismatches    43:  Indels     17:  Gaps       6:

OY      7 FOQRHI-----INPPIICNTIMDNINIYVGQCKRVTFFIISATVKAICTGV-INMN 59
|||::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
DB      8 FQRHMDDSSSSNSNNCLNLMRSR--NMGGRCRKPVTFFHESLADVAQCSDINWCK 66
||||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
OY      60 VLSTFRPOLNT-----CTRTSTPRP-CPYSSRTETNYICVKCENQ--YVHPF 104
|||::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
DB      67 NGOTNCYSNSTMTHTDCCRQTGSSSKYPNCAYKASOEOKHIIIVACEGNPPVPVHF 120
||||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

RESULT 9
S41111
pancreatic ribonuclease - common Iguana
C:Species: Iguana iguana (common Iguana)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C:Accession: S41111
R:Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A>Title: The amino acid sequence of Iguana (Iguana iguana) pancreatic ribonuclease.
A:Reference number: S41111; MUID:94139745; PMID:8307028
A:Accession: S41111
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-119 <ZHA>
C:Superfamily: pancreatic ribonuclease

Query Match          20.7%   Score 125.5 : DB 2 : Length 119:
Best Local Similarity 29.6%   Pred. No. 1.2e+05:
Matches      34:  Conservative    16:  Mismatches    52:  Indels     13:  Gaps       4:

OY      2 QNWATFOQKH-----INPPIICNTIMDNINIYVGQCKRVTFIFIISATVKAIC-- 52
|||::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
DB      1 QDWSEFOKHIDYDETSASNPNAYCDLMMQR--NLNPFKCKTRMFPVHASSSEIQVCGS 59
||||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
OY      53 --TGVINNVNLTSTRFOLNTCTRITSIT-PRCPPISSRTETNYICVKCENQVPVF 104
|||::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
DB      60 GGTVEEDNLVDSNESFDLTDCKNVGFAPSSCKNGTPGTRIRIACENNPPVHF 114
||||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

RESULT 10
NRPRH
pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: Antilocapra americana (pronghorn)
C:Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
C:Accession: A00813
R:Beintema, J.J.; Gaastria, W.; Munniksma, J.
J. Mol. Evol. 13, 305-316, 1979
A>Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship b
A:Reference number: A00813; MUID:80075014; PMID:513141
A:Accession: A00813
A:Molecule type: protein
A:Residues: 1-124 <BET>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match          19.2%   Score 116.5 : DB 1 : Length 124:
Best Local Similarity 29.4%   Pred. No. 9.9e+05:
Matches      35:  Conservative    18:  Mismatches    43:  Indels     23:  Gaps       7:

OY      5 ATPQKHINPI-----ICNTIMDNINIYVGQCKRVTFFIISATTVKAICTGVINM 58
|||::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

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Db 6 AKEROHIDNSSVSSNYCNQMKSR-NLQGRCKPVNTFVHESLADVOAVCS---OK 61  
QY 59 NVL-----STTRFOLNCTRTSTTPRP-CPYSSRTETNYICVCE-NQY-PVHF 104  
Db 62 NVACKNGQTCNQYQISITMSITPCRETGSSKRYNCARKTQAKHIIIVACEGPNYPVHF 120

## RESULT 11

pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo

N:Alternate names: RNase A  
C:Species: *Macropus rufus*, *Megaleia rufa* (red kangaroo)  
C:Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 04-Oct-1996  
C:Accession: A00833  
R:Gaastera, W.; Welling, G.W.; Beintema, J.J.  
Eur. J. Biochem. 86, 209-217, 1978  
A:Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.  
A:Reference number: A00833; MUID:78190621; PMID:658039  
A:Accession: A00833  
A:Molecule type: protein  
A:Residues: 1-122 <GAA>

C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:11-40,117/Active site: His, Lys, His #status predicted  
F:25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted  
F:61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 19.1%; Score 116; DB 1; Length 122;  
Best Local Similarity 29.8%; Pred. No. 0.00011;  
Matches 34; Conservative 16; Mismatches 46; Indels 18; Gaps 6;

QY 7 FQOKHI-----INPILCTIMDNIIYVGQCKRVTFIISATYKAIC----- 52  
Db 7 FQROHMDTEHSTASSNYCNLMKAR-DMTSGCRKPLMTFIEPKSVYDVACHQENWCK 65  
QY 53 TGVIMANLSTTRFOLNCTRTSTTPRP-CPYSSRTETNYICVCE-NQY-PVHF 104  
Db 66 NGRTNC-YKSNRSLSTNCRQTAGSKRYPCQYETSLNKLQIIIVACEGQYVPVHF 118

## RESULT 12

NCRU

pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)  
N:Alternate names: RNase 1; RNase A  
C:Species: *Myocastor coypus* (nutria, coypu)  
C:Date: 24-Apr-1984 #sequence\_revision 30-Sep-1988 #text\_change 31-Mar-2000  
C:Accession: A00822  
R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.  
Biochim. Biophys. Acta 453, 400-409, 1976  
A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic  
A:Reference number: A90612; MUID:77065676; PMID:999896  
A:Accession: A00822  
A:Molecule type: protein  
A:Residues: 1-128 <VAN>

C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:12-41,119/Active site: His, Lys, His #status predicted  
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 18.9%; Score 114.5; DB 1; Length 128;  
Best Local Similarity 30.8%; Pred. No. 0.00016;  
Matches 36; Conservative 15; Mismatches 43; Indels 23; Gaps 7;

QY 7 FQOKHI-----INPILCTIMDNIIYVGQCKRVTFIISATYKAICGTGINNV 60  
Db 8 FERQHMDSRSPSTNPVNCNEMKSR-NMTGRCRKPVTFEVHEPLADVOAVC---FQKNV 63  
QY 61 L-----STTRFOLNCTRTSTTPRP-CPYSSRTETNYICVCE-NQY-PVHF 104  
Db 64 LCKNGQTCNQYQISITMSITPCRETGSSKRYNCARKTQAKHIIIVACEGPNYPVHF 120

## RESULT 13

NRMS

pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse

N:Alternate names: RNase 1; RNase A  
C:Species: *Mus musculus* (house mouse)  
C:Date: 30-Nov-1980 #sequence\_revision 13-Mar-1997 #text\_change 18-Jun-1999  
C:Accession: A34090; S22598; A00830  
R:Schueller, C.; Mijssen, H.M.J.; Kok, R.; Beintema, J.J.  
Mol. Biol. Evol. 7, 29-44, 1990  
A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mo  
A:Reference number: A34090; MUID:90136034; PMID:2299980  
A:Accession: A34090  
A:Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-149 <SCH>  
A:Cross-references: GB:M27814; NID:9200762; PIDN:AAA40060.1; PID:9200763  
R:Samuelson, L.C.; Wiedauer, K.; Howard, G.; Schmidt, R.M.; Koeplin, D.; Weisler, M.H.  
Nucleic Acids Res. 19, 6935-6941, 1991  
A:Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specif  
A:Reference number: S22598; MUID:92107684; PMID:1840677  
A:Accession: S22598  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-149 <SAA>  
A:Cross-references: EMBL:X60103; NID:953981; PIDN:CAA42697.1; PID:953982  
R:Lenstra, J.A.; Beintema, J.J.  
Eur. J. Biochem. 98, 399-408, 1979  
A:Title: The amino acid sequence of mouse pancreatic ribonuclease.  
A:Reference number: A00830; MUID:80024269; PMID:556267  
A:Accession: A00830  
A:Molecule type: protein  
A:Residues: 26-149 <LEN>

C:Superfamily: pancreatic ribonuclease  
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
F:1-25/Domain: signal sequence #status predicted <Sig>  
F:26-149/Product: pancreatic ribonuclease #status predicted <MAT>  
F:37,66,144/Active site: His, Lys, His #status predicted  
F:51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted  
F:62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.9%; Score 114.5; DB 1; Length 149;  
Best Local Similarity 29.9%; Pred. No. 0.00019;  
Matches 35; Conservative 16; Mismatches 43; Indels 23; Gaps 7;

QY 7 FQOKHI-----INPILCTIMDNIIYVGQCKRVTFIISATYKAICGTGINNV 60  
Db 33 FQROHMDDGSSINSPTFCNOMKRR-DMTGSCRKPVTFEVHEPLADVOAVCS---QENV 88  
QY 61 L-----STTRFOLNCTRTSTTPRP-CPYSSRTETNYICVCE-NQY-PVHF 104  
Db 89 TCKNRKSMCYKSSSLHITDCHLKGNSKRYPCQYKTTQYQKHIIIVACEGPNYPVHF 145

## RESULT 14

A43825

angiotensin - pig

C:Species: *Sus scrofa domestica* (domestic pig)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S29834; A43825  
R:Bond, M.D.; Strydom, D.J.; Vallee, B.L.  
Biochim. Biophys. Acta 1162, 177-186, 1993  
A:Title: Characterization and sequencing of rabbit, pig and mouse angiotensin: discer  
A:Reference number: S29833; MUID:93192291; PMID:8448182  
A:Accession: S29834  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-123 <BON>

A:Note: this sequence was submitted to the Protein Sequence Database, December 1992  
C:Superfamily: pancreatic ribonuclease

Query Match 18.7%; Score 113.5; DB 1; Length 123;  
Best Local Similarity 38.2%; Pred. No. 0.0002;  
Matches 29; Conservative 6; Mismatches 36; Indels 5; Gaps 2;



